

We claim:

1. A substantially purified nucleic acid molecule that encodes a maize or soybean tocopherol synthesis pathway enzyme or fragment thereof, wherein said maize or soybean tocopherol synthesis pathway enzyme is selected from the group consisting of:

- 5 (a) deoxyarabiono-heptulosonate-P-synthase or fragment thereof;
- (b) putative deoxyarabiono-heptulosonate-P-synthase or fragment thereof;
- (c) dehydroquinase synthase or fragment thereof;
- (d) dehydroquinase dehydratase or fragment thereof;
- (e) putative dehydroquinase dehydratase or fragment thereof;
- 10 (f) shikimate dehydrogenase or fragment thereof;
- (g) shikimate kinase or fragment thereof;
- (h) enolpyruvylshikimate-P-synthase or fragment thereof;
- (i) chorismate synthase or fragment thereof;
- (j) chorismate mutase or fragment thereof;
- 15 (k) tyrosine transaminase or fragment thereof;
- (l) putative tyrosine transaminase or fragment thereof;
- (m) transaminase A or fragment thereof;
- (n) putative transaminase A or fragment thereof;
- (o) 4-hydroxyphenylpyruvate dioxygenase or fragment thereof;
- 20 (p) homogentisic acid dioxygenase or fragment thereof; and
- (q) geranylgeranylpyrophosphate synthase or fragment thereof.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 627.

3. A substantially purified maize or soybean tocopherol synthesis pathway enzyme or
5 fragment thereof, wherein said maize or soybean tocopherol synthesis pathway enzyme is selected from the group consisting of:

- (a) deoxyarabiono-heptulosonate-P-synthase or fragment thereof;
- (b) putative deoxyarabiono-heptulosonate-P-synthase or fragment thereof;
- (c) dehydroquinase synthase or fragment thereof;
- (d) dehydroquinase dehydratase or fragment thereof;
- (e) putative dehydroquinase dehydratase or fragment thereof;
- (f) shikimate dehydrogenase or fragment thereof;
- (g) shikimate kinase or fragment thereof;
- (h) enolpyruvylshikimate-P-synthase or fragment thereof;
- (i) chorismate synthase or fragment thereof;
- (j) chorismate mutase or fragment thereof;
- (k) tyrosine transaminase or fragment thereof;
- (l) putative tyrosine transaminase or fragment thereof;
- (m) transaminase A or fragment thereof;
- (n) putative transaminase A or fragment thereof;
- (o) 4-hydroxyphenylpyruvate dioxygenase or fragment thereof;
- (p) homogentisic acid dioxygenase or fragment thereof; and

(q) geranylgeranylpyrophosphate synthase or fragment thereof.

4. A substantially purified maize or soybean tocopherol synthesis pathway enzyme or fragment thereof according to claim 3, wherein said maize or soybean tocopherol synthesis

5 pathway enzyme or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 627.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize or soybean tocopherol synthesis pathway enzyme or fragment thereof according to claim 4.

10 6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

15 (a) a nucleic acid sequence which encodes for a deoxyarabiono-heptulosonate-P-synthase enzyme or fragment thereof;

(b) a nucleic acid sequence which encodes for a putative deoxyarabiono-heptulosonate-P-synthase enzyme or fragment thereof;

20 (c) a nucleic acid sequence which encodes for a dehydroquinate synthase enzyme or fragment thereof;

(d) a nucleic acid sequence which encodes for a dehydroquate dehydratase enzyme or fragment thereof;

(e) a nucleic acid sequence which encodes for a putative dehydroquate dehydratase enzyme or fragment thereof;

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(f) a nucleic acid sequence which encodes for a shikimate dehydrogenase enzyme or fragment thereof;

(g) a nucleic acid sequence which encodes for a shikimate kinase enzyme or fragment thereof;

(h) a nucleic acid sequence which encodes for an enolpyruvylshikimate-P-synthase enzyme or fragment thereof;

(i) a nucleic acid sequence which encodes for a chorismate synthase enzyme or fragment thereof;

(j) a nucleic acid sequence which encodes for a chorismate mutase enzyme or fragment thereof;

(k) a nucleic acid sequence which encodes for a tyrosine transaminase enzyme or fragment thereof;

(l) a nucleic acid sequence which encodes for a putative Tyrosine transaminase enzyme or fragment thereof;

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(m) a nucleic acid sequence which encodes for a transaminase A enzyme or fragment thereof;

(n) a nucleic acid sequence which encodes for a putative transaminase A enzyme or fragment thereof;

(o) a nucleic acid sequence which encodes for a 4-hydroxyphenylpyruvate dioxygenase enzyme or fragment thereof;

(p) a nucleic acid sequence which encodes for a homogentisic acid dioxygenase enzyme or fragment thereof; and

5 (q) a nucleic acid sequence which encodes for a geranylgeranylpyrophosphate synthase enzyme or fragment thereof;

(r) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (q); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

10 7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (q).

15 8. A method for determining a level or pattern in a plant cell of a tocopherol synthesis pathway enzyme in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 627 or complements thereof, with a
20 complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary

nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said tocopherol synthesis pathway enzyme;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

5 (C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said tocopherol synthesis pathway enzyme in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.

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